RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _09/037,657B_

Source: _1 Fw/6_

Date Processed by STIC: _7/20/06_

ENTERED

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         RAW SEQUENCE LISTING              DATE: 07/20/2006
         PATENT APPLICATION:  US/09/037,657B      TIME: 16:44:14

         Input Set : A:\10857Z.SEQ.txt
         Output Set: N:\CRF4\07202006\I037657B.raw


    4 <110> APPLICANT: Hilton, Douglas J.
    5        Nicola, Nicos A.
    6        Farley, Alison
    7        Wilson, Tracy
    8        Zhang, Jian-Guo
    9        Alexander, Warren
   10        Rakar, Steven
   11        Fabri, Louis
   12        Kojima, Tetsuo
   13        Maeda, Masatsugu
   14        Kikuchi, Yasufumi
   15        Nash, Andrew
   17 <120> TITLE OF INVENTION: A NOVEL HAEMPOIETIN RECEPTOR AND GENETIC SEQUENCES
   18        ENCODING SAME
   20 <130> FILE REFERENCE: DAVIES COLLISON CAVE (CIP)
   22 <140> CURRENT APPLICATION NUMBER: 09/037,657B
   23 <141> CURRENT FILING DATE: 1998-03-10
   25 <150> PRIOR APPLICATION NUMBER: 08/928,720
   26 <151> PRIOR FILING DATE: 1997-09-11
   28 <160> NUMBER OF SEQ ID NOS: 58
   30 <170> SOFTWARE: PatentIn Ver. 2.0
   32 <210> SEQ ID NO: 1
   33 <211> LENGTH: 5
   34 <212> TYPE: PRT
   35 <213> ORGANISM: Unknown
   37 <220> FEATURE:
   38 <223> OTHER INFORMATION: Description of Unknown Organism: haemopoietin receptor
   40 <220> FEATURE:
   41 <221> NAME/KEY: UNSURE
   42 <222> LOCATION: (3)
   43 <223> OTHER INFORMATION: Unsure at position 3
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W--> 46 Trp Ser Xaa Trp Ser
   47     1               5
   50 <210> SEQ ID NO: 2
   51 <211> LENGTH: 24
   52 <212> TYPE: DNA
   53 <213> ORGANISM: Artificial Sequence
   55 <220> FEATURE:
   56 <223> OTHER INFORMATION: Description of Artificial Sequence: M116 probe
   59 <400> SEQUENCE: 2
   60 actcgctcca gattcccgcc tttt                          24
   63 <210> SEQ ID NO: 3
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 64 <211> LENGTH: 24
 65 <212> TYPE: DNA
 66 <213> ORGANISM: Artificial Sequence
 68 <220> FEATURE:
 69 <223> OTHER INFORMATION: Description of Artificial Sequence:M108 probe
 71 <400> SEQUENCE: 3
 72 tcccgccttt ttcgacccat agat                                    24
 75 <210> SEQ ID NO: 4
 76 <211> LENGTH: 24
 77 <212> TYPE: DNA
 78 <213> ORGANISM: Artificial Sequence
 80 <220> FEATURE:
 81 <223> OTHER INFORMATION: Description of Artificial Sequence:M159 probe
 83 <400> SEQUENCE: 4
 84 ggtacttggc ttggaagagg aaat                                    24
 87 <210> SEQ ID NO: 5
 88 <211> LENGTH: 24
 89 <212> TYPE: DNA
 90 <213> ORGANISM: Artificial Sequence
 92 <220> FEATURE:
 93 <223> OTHER INFORMATION: Description of Artificial Sequence:M242 probe
 95 <400> SEQUENCE: 5
 96 cggctcacgt gcacgtcggg tggg                                    24
 99 <210> SEQ ID NO: 6
100 <211> LENGTH: 22
101 <212> TYPE: DNA
102 <213> ORGANISM: Artificial Sequence
104 <220> FEATURE:
105 <223> OTHER INFORMATION: Description of Artificial Sequence:M112 probe
107 <400> SEQUENCE: 6
108 agctgctgtt aaagggcttc tc                                      22
111 <210> SEQ ID NO: 7
112 <211> LENGTH: 15
113 <212> TYPE: DNA
114 <213> ORGANISM: Unknown
117 <220> FEATURE:
118 <223> OTHER INFORMATION: Description of Unknown Organism:Unsure
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122 <222> LOCATION: (1)
123 <223> OTHER INFORMATION: Unsure at position 1
125 <220> FEATURE:
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130 <220> FEATURE:
131 <221> NAME/KEY: unsure
132 <222> LOCATION: (10)
133 <223> OTHER INFORMATION: Unsure at position 10
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135 <400> SEQUENCE: 7
136 rctccartcr ctcca                                              15
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142 <213> ORGANISM: Unknown
144 <220> FEATURE:
145 <223> OTHER INFORMATION: Description of Unknown Organism:Unsure
147 <220> FEATURE:
148 <221> NAME/KEY: unsure
149 <222> LOCATION: (1)
150 <223> OTHER INFORMATION: Unsure at position 1
152 <220> FEATURE:
153 <221> NAME/KEY: unsure
154 <222> LOCATION: (7)
155 <223> OTHER INFORMATION: Unsure at position 7
157 <220> FEATURE:
158 <221> NAME/KEY: unsure
159 <222> LOCATION: (10)
160 <223> OTHER INFORMATION: Unsure at position 10
162 <400> SEQUENCE: 8
163 rctccaytcr ctcca                                              15
166 <210> SEQ ID NO: 9
167 <211> LENGTH: 21
168 <212> TYPE: DNA
169 <213> ORGANISM: Artificial Sequence
171 <220> FEATURE:
172 <223> OTHER INFORMATION: Description of Artificial Sequence:1944 probe
174 <400> SEQUENCE: 9
175 aagtgtgacc atcatgtgga c                                       21
178 <210> SEQ ID NO: 10
179 <211> LENGTH: 18
180 <212> TYPE: DNA
181 <213> ORGANISM: Artificial Sequence
183 <220> FEATURE:
184 <223> OTHER INFORMATION: Description of Artificial Sequence:2106 probe
186 <400> SEQUENCE: 10
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190 <210> SEQ ID NO: 11
191 <211> LENGTH: 18
192 <212> TYPE: DNA
193 <213> ORGANISM: Artificial Sequence
195 <220> FEATURE:
196 <223> OTHER INFORMATION: Description of Artificial Sequence:2120 probe
198 <400> SEQUENCE: 11
199 atgcccgcgg gtcgcccg                                           18
202 <210> SEQ ID NO: 12
203 <211> LENGTH: 1629
204 <212> TYPE: DNA
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Input Set : A:\10857Z.SEQ.txt
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205 <213> ORGANISM: Unknown
207 <220> FEATURE:
208 <221> NAME/KEY: CDS
209 <222> LOCATION: (124)..(1362)
211 <220> FEATURE:
212 <223> OTHER INFORMATION: Description of Unknown Organism:Murine NR6.1
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215 ggcacgagct tcgctgtccg cgcccagtga cgcgcgtgcg gacccgagcc ccaatctgca 60
217 ccccgcagac tcgcccccgc cccataccgg cgttgcagtc accgcccgtt gcgcgccacc 120
219 ccc atg ccc gcg ggt cgc ccg ggc ccc gtc gcc caa tcc gcg cgg cgg   168
220   Met Pro Ala Gly Arg Pro Gly Pro Val Ala Gln Ser Ala Arg Arg
221   1   5   10   15
223 ccg ccg cgg ccg ctg tcc tcg ctg tgg tcg cct ctg ttg ctc tgt gtc   216
224 Pro Pro Arg Pro Leu Ser Ser Leu Trp Ser Pro Leu Leu Leu Cys Val
225   20   25   30
227 ctc ggg gtg cct cgg ggc gga tcg gga gcc cac aca gct gta atc agc   264
228 Leu Gly Val Pro Arg Gly Gly Ser Gly Ala His Thr Ala Val Ile Ser
229   35   40   45
231 ccc cag gac ccc acc ctt ctc atc ggc tcc tcc ctg caa gct acc tgc   312
232 Pro Gln Asp Pro Thr Leu Leu Ile Gly Ser Ser Leu Gln Ala Thr Cys
233   50   55   60
235 tct ata cat gga gac aca cct ggg gcc acc gct gag ggg ctc tac tgg   360
236 Ser Ile His Gly Asp Thr Pro Gly Ala Thr Ala Glu Gly Leu Tyr Trp
237   65   70   75
239 acc ctc aat ggt cgc cgc ctg ccc tct gag ctg tcc cgc ctc ctt aac   408
240 Thr Leu Asn Gly Arg Arg Leu Pro Ser Glu Leu Ser Arg Leu Leu Asn
241 80   85   90   95
243 acc tcc acc ctg gcc ctg gcc ctg gct aac ctt aat ggg tcc agg cag   456
244 Thr Ser Thr Leu Ala Leu Ala Leu Ala Asn Leu Asn Gly Ser Arg Gln
245   100   105   110
247 cag tca gga gac aat ctg gtg tgt cac gcc cga gac ggc agc att ctg   504
248 Gln Ser Gly Asp Asn Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu
249   115   120   125
251 gct ggc tcc tgc ctc tat gtt ggc ttg ccc cct gag aag ccc ttt aac   552
252 Ala Gly Ser Cys Leu Tyr Val Gly Leu Pro Pro Glu Lys Pro Phe Asn
253   130   135   140
255 atc agc tgc tgg tcc cgg aac atg aag gat ctc acg tgc cgc tgg aca   600
256 Ile Ser Cys Trp Ser Arg Asn Met Lys Asp Leu Thr Cys Arg Trp Thr
257   145   150   155
259 ccg ggt gca cac ggg gag aca ttc tta cat acc aac tac tcc ctc aag   648
260 Pro Gly Ala His Gly Glu Thr Phe Leu His Thr Asn Tyr Ser Leu Lys
261 160   165   170   175
263 tac aag ctg agg tgg tac ggt cag gat aac aca tgt gag gag tac cac   696
264 Tyr Lys Leu Arg Trp Tyr Gly Gln Asp Asn Thr Cys Glu Glu Tyr His
265   180   185   190
267 act gtg ggc cct cac tca tgc cat atc ccc aag gac ctg gcc ctc ttc   744
268 Thr Val Gly Pro His Ser Cys His Ile Pro Lys Asp Leu Ala Leu Phe
269   195   200   205
271 act ccc tat gag atc tgg gtg gaa gcc acc aat cgc cta ggc tca gca   792

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272 Thr Pro Tyr Glu Ile Trp Val Glu Ala Thr Asn Arg Leu Gly Ser Ala
273         210             215             220
275 aga tct gat gtc ctc aca ctg gat gtc ctg gac gtg gtg acc acg gac   840
276 Arg Ser Asp Val Leu Thr Leu Asp Val Leu Asp Val Val Thr Thr Asp
277     225             230             235
279 ccc cca ccc gac gtg cac gtg agc cgc gtt ggg ggc ctg gag gac cag   888
280 Pro Pro Pro Asp Val His Val Ser Arg Val Gly Gly Leu Glu Asp Gln
281 240             245             250                 255
283 ctg agt gtg cgc tgg gtc tca cca cca gct ctc aag gat ttc ctc ttc   936
284 Leu Ser Val Arg Trp Val Ser Pro Pro Ala Leu Lys Asp Phe Leu Phe
285             260             265             270
287 caa gcc aag tac cag atc cgc tac cgc gtg gag gac agc gtg gac tgg   984
288 Gln Ala Lys Tyr Gln Ile Arg Tyr Arg Val Glu Asp Ser Val Asp Trp
289         275             280             285
291 aag gtg gtg gat gac gtc agc aac cag acc tcc tgc cgt ctc gcg ggc  1032
293 Lys Val Val Asp Asp Val Ser Asn Gln Thr Ser Cys Arg Leu Ala Gly
294         290             295             300
296 ctg aag ccc ggc acc gtt tac ttc gtc caa gtg cgt tgt aac cca ttc  1080
297 Leu Lys Pro Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe
298     305             310             315
300 ggg atc tat ggg tcg aaa aag gcg gga atc tgg agc gag tgg agc cac  1128
301 Gly Ile Tyr Gly Ser Lys Lys Ala Gly Ile Trp Ser Glu Trp Ser His
302 320             325             330                 335
304 ccc acc gct gcc tcc acc cct cga agt gag cgc ccg ggc ccg ggc ggc  1176
305 Pro Thr Ala Ala Ser Thr Pro Arg Ser Glu Arg Pro Gly Pro Gly Gly
306             340             345             350
308 ggg gtg tgc gag ccg cgg ggc ggc gag ccc agc tcg ggc ccg gtg cgg  1224
309 Gly Val Cys Glu Pro Arg Gly Gly Glu Pro Ser Ser Gly Pro Val Arg
310             355             360             365
312 cgc gag ctc aag cag ttc ctc ggc tgg ctc aag aag cac gca tac tgc  1272
313 Arg Glu Leu Lys Gln Phe Leu Gly Trp Leu Lys Lys His Ala Tyr Cys
314         370             375             380
316 tcg aac ctt agt ttc cgc ctg tac gac cag tgg cgt gct tgg atg cag  1320
317 Ser Asn Leu Ser Phe Arg Leu Tyr Asp Gln Trp Arg Ala Trp Met Gln
318     385             390             395
320 aag tca cac aag acc cga aac cag gtc ctg ccg gct aaa ctc           1362
321 Lys Ser His Lys Thr Arg Asn Gln Val Leu Pro Ala Lys Leu
322 400             405             410
324 taaggatagg ccatcctcct gctgggtcag acctggaggc tcacctgaat tggagcccct 1422
326 ctgtaccatc tgggcaacaa agaaacctac cagaggctgg ggcacaatga gctcccacaa 1482
328 ccacagcttt ggtccacatg atggtcacac ttggatatac cccagtgtgg gtaaggttgg 1542
330 ggtattgcag ggcctcccaa caatctcttt aaataaataa aggagttgtt caggtaaaaa 1602
332 aaaaaaaaaa aaaaaaaaaa aaaaaaa                                     1629
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335 <210> SEQ ID NO: 13
336 <211> LENGTH: 413
337 <212> TYPE: PRT
338 <213> ORGANISM: Unknown
340 <220> FEATURE:
341 <223> OTHER INFORMATION: Description of Unknown Organism:Murine NR6.1

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 07/20/2006
PATENT APPLICATION: US/09/037,657B   TIME: 16:44:15

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Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos. 3
Seq#:29; Xaa Pos. 136,139,162,177

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:21; Line(s) 949

Invalid <213> Response:
Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:45